Package 'hetsurrSurv'

June 15, 2023

Type Package

Title Assessing Heterogeneity in Surrogacy Using Censored Data

Version 1.0

Date 2023-06-01

Author Layla Parast

Maintainer Layla Parast <parast@austin.utexas.edu>

Description Provides functions to assess and test for heterogeneity in the utility of a surrogate marker with respect to a baseline covariate using censored (survival data), and to test for heterogeneity across multiple time points. More details will be available in the future in: Parast, L., Tian L, Cai, T. (2023) ``Assessing Heterogeneity in Surrogacy Using Censored Data." Under Review.

License GPL

Imports stats, Rsurrogate, MASS, groc

NeedsCompilation no

Depends R (>= 3.5.0)

R topics documented:

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example.data   *Example data*

Description

Example data

Usage

```
data("example.data")
```

Format

A list with 8 elements representing 2000 observations from a treatment group and 1500 observations from a control group:

s1 the surrogate marker in the treatment group

s0 the surrogate marker in the control group

w1 the baseline covariate of interest in the treatment group

w0 the baseline covariate of interest in the control group

d1 the event indicator in the treatment group

d0 the event indicator in the control group

x1 the observed event time in the treatment group

x0 the observed evenet time in the control group

Examples

```
data(example.data)
names(example.data)
```

R.main.estimate	*Estimates the proportion of treatment effect explained by the surrogate marker as a function of a baseline covariate*

Description

Assesses heterogeneity in the utility of a surrogate marker with respect to a baseline covariate using censored (survival data) by estimates the proportion of treatment effect explained by the surrogate marker as a function of a baseline covariate, w

Usage

```
R.main.estimate(xone, xzero, deltaone, deltazero, sone, szero, wone, wzero, w.grd, myt,
landmark, type = "cont", var = FALSE, test = FALSE, extrapolate = T, h.0 = NULL,
h.1 = NULL, h.w = NULL, h.s = NULL, h.w.1 = NULL)
```

Arguments

xone	x1, observed event time in the treated group
xzero	x0, observed event time in the control group
deltaone	delta1, event indicator in the treated group
deltazero	delta0, event indicator in the control group
sone	s1, surrogate marker in the treated group
szero	s0, surrogate marker in the control group
wone	w1, baseline covariate in the treated group
wzero	w0, baseline covariate in the control group
w.grd	grid for w where estimation will be provided
myt	t of interest

landmark	t0, landmark time
type	options are "cont" or "discrete"; type of baseline covariate, default is "cont"
var	TRUE or FALSE, if variance/standard error estimates are wanted
test	TRUE or FALSE, if test for heterogeneity is wanted wanted
extrapolate	TRUE or FALSE
h.0	bandwidth
h.1	bandwidth
h.w	bandwidth
h.s	bandwidth
h.w.1	bandwidth

Value

A list is returned:

w.values	grid for w where estimation is provided
R.s.w	The propoportion of treatment effect explained as a function of the baseline covariate, w
delta.w	The treatment effect as a function of the baseline covariate, w
delta.s.w	The residual treatment effect as a function of the baseline covariate, w
sd.R	Standard error estimate of R.s.w
sd.delta	Standard error estimate of delta.w
sd.delta.s	Standard error estimate of delta.s.w
pval.omnibus	p-value from the omnibus test for heterogeneity
pval.con	p-value from the conservative omnibus test for heterogeneity

Author(s)

Layla Parast

References

Parast, L., Tian L, Cai, T. (2023) "Assessing Heterogeneity in Surrogacy Using Censored Data." Under Review.

Examples

```
data(example.data)
names(example.data)
R.main.estimate(xone=example.data$x1, xzero=example.data$x0, deltaone=example.data$d1, deltazero=example.dat
#computationally intensive

R.main.estimate(xone=example.data$x1, xzero=example.data$x0, deltaone=example.data$d1, deltazero=example.dat
```

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test.multiplet *Tests for heterogeneity across multiple timepoints*

Description

Tests for heterogeneity across multiple timepoints

Usage

```
test.multiplet(t.mult, xone, xzero, deltaone, deltazero, sone, szero, wone,
wzero, w.grd, landmark, extrapolate = T, h.0 = NULL, h.1 = NULL, h.w = NULL,
h.s = NULL, h.w.1 = NULL)
```

Arguments

t.mult	Vector of time points
xone	x1, observed event time in the treated group
xzero	x0, observed event time in the control group
deltaone	delta1, event indicator in the treated group
deltazero	delta0, event indicator in the control group
sone	s1, surrogate marker in the treated group
szero	s0, surrogate marker in the control group
wone	w1, baseline covariate in the treated group
wzero	w0, baseline covariate in the control group
w.grd	grid for w where estimation will be provided
landmark	t0, landmark time
extrapolate	TRUE or FALSE
h.0	bandwidth
h.1	bandwidth
h.w	bandwidth
h.s	bandwidth
h.w.1	bandwidth

Value

A list is returned:

pval.multi	p-value for omnibus test
pval.con.multi	p-value for conservative omnibus test

Author(s)

Layla Parast

References

Parast, L., Tian L, Cai, T. (2023) "Assessing Heterogeneity in Surrogacy Using Censored Data."
Under Review.

Examples

```
data(example.data)
names(example.data)
#computationally intensive

test.multiplet(t.mult = c(1,1.25,1.5), xone=example.data$x1, xzero=example.data$x0, deltaone=example.data$d1
```

Index